Amendments to the Claims

1. (Currently Amended) A hybridization assay probe comprising ~~an oligonucleotide which~~ a target binding region from 18 to 35 bases in length that hybridizes to a target sequence present in target nucleic acid derived from a *Cryptosporidium parvum* organism in a test sample under stringent conditions to form a probe:target hybrid stable for detection, ~~said oligonucleotide having an at least 10 contiguous base region which is at least 80% complementary to an at least 10 contiguous base region present in the target sequence, wherein~~ the said target sequence ~~is~~ being selected from the group consisting of SEQ ID NO:6, SEQ ID NO:10, SEQ ID NO:14 and SEQ ID NO:18, wherein said probe does not comprise a base region in addition to said target binding region that is capable of stably binding to said target nucleic acid under said conditions, and wherein said probe does not hybridize to nucleic acid derived from a *Cryptosporidium muris*, *Cryptosporidium baileyi* or ~~*Crptosporidium*~~ *Cryptosporidium wrairi* organism ~~in the test sample~~ to form a probe:non-target hybrid stable for detection under the said stringent conditions.

Claims 2-10 (Canceled)

11. (Currently Amended) The probe of claim 1, wherein said probe contains at least two base ~~sequences which~~ regions that hybridize to each other when said probe is not hybridized to ~~the~~ said target sequence under ~~the stringent~~ said conditions.

12. (Currently Amended) The probe of claim 1, wherein said probe comprises ~~one or more~~ at least one base ~~sequences which do~~ region that does not stably hybridize to nucleic acid derived from a *Cryptosporidium parvum* organism, ~~or to nucleic acid derived from a non-target organism present in the test sample,~~ under ~~the stringent~~ said conditions.

13. Canceled

14. (Original) The probe of claim 1 further comprising a detectable label.

15. (Currently Amended) The probe of claim ~~1~~ 11 further comprising a group of interacting labels.

16. (Original) The probe of claim 15, wherein said interacting labels include a luminescent label and a quencher label.

17. (Currently Amended) The probe of claim 1, wherein said ~~oligonucleotide~~ target binding region includes at least one ribonucleotide modified to include a 2'-O-methyl substitution to the ribofuranosyl moiety.

18. (Currently Amended) The probe of claim 1, wherein a pseudo peptide backbone joins at least a portion of the bases of said ~~oligonucleotide~~ target binding region.

19. (Currently Amended) The probe of claim 1, wherein ~~the stringent~~ said conditions comprise 100 mM succinic acid, 2% (w/v) LLS, 15 mM aldrithiol-2, 1.2 M LiCl, 20 mM EDTA, 3% (v/v) ethyl alcohol (absolute), pH 4.7, and a test sample temperature of about 60°C.

20. (Currently Amended) ~~A hybridization assay~~ The probe of claim 1, ~~comprising an oligonucleotide which hybridizes to a target sequence present in nucleic acid derived from a *Cryptosporidium parvum* organism in a test sample under stringent conditions to form a probe:target hybrid stable for detection, said oligonucleotide having a~~ wherein the base sequence ~~which~~ of said target binding region is at least 80% complementary to the base sequence of the said target sequence;

~~wherein the target sequence has a base sequence selected from the group consisting of SEQ ID NO:6, SEQ ID NO:10, SEQ ID NO:14 and SEQ ID NO:18, and wherein said probe does not hybridize to nucleic acid derived from a *Cryptosporidium muris*, *Cryptosporidium baileyi* or *Crptosporidium wrairi* organism in the test sample to form a probe:non-target hybrid stable for detection under the stringent conditions.~~

21. (Currently Amended) ~~An oligonucleotide~~ The probe of claim 1, ~~which hybridizes to a target sequence present in nucleic acid derived from a *Cryptosporidium parvum* organism in a test sample under stringent conditions to form a probe:target hybrid stable for detection;~~ wherein the base sequence of said probe is at least 80% complementary to the base sequence of ~~the~~ said target sequence, ~~wherein the target sequence is selected from the group consisting of SEQ ID NO:6, SEQ ID NO:10, SEQ ID NO:14 and SEQ ID NO:18, and wherein said probe does not hybridize to nucleic acid derived from a *Cryptosporidium muris*, *Cryptosporidium baileyi* or *Crptosporidium wrairi* organism in the test sample to form a probe:non-target hybrid stable for detection under the stringent conditions.~~

22. (Currently Amended) ~~An oligonucleotide~~ The probe of claim 1, ~~which hybridizes to a target sequence present in nucleic acid derived from a *Cryptosporidium parvum* organism in a test sample under stringent conditions to form a probe:target hybrid stable for detection;~~ wherein the base sequence of said probe is fully complementary to the base sequence of ~~the~~ said target sequence, ~~wherein the target sequence is selected from the group consisting of SEQ ID NO:6 SEQ ID NO:10, SEQ ID NO:14 and SEQ ID NO:18, and wherein said probe does not hybridize to nucleic acid derived from a *Cryptosporidium muris*, *Cryptosporidium baileyi* or *Crptosporidium wrairi* organism in the test sample to form a probe:non-target hybrid stable for detection under the stringent conditions.~~

23. (Currently Amended) A probe mix comprising ~~the~~ said probe of claim 1 and a first helper oligonucleotide from 18 to 35 bases in length that hybridizes to ~~having an at least 10 contiguous base region which is at least 80% complementary to an at least 10 contiguous base region present in~~ a target sequence selected from the group consisting of SEQ ID NO:29, SEQ ID NO:33, SEQ ID NO:37 and SEQ ID NO:41 under stringent conditions.

Claims 24-28 (Canceled)

29. (Currently Amended) The probe mix of claim 23 further comprising a second helper oligonucleotide from 18 to 35 bases in length that hybridizes to ~~having an at least 10 contiguous base region which is at least 80% complementary to an at least 10 contiguous base region present in~~ a target sequence selected from the group consisting of SEQ ID NO:32, SEQ ID NO:36, SEQ ID NO:40 and SEQ ID NO:44 under stringent conditions.

Claims 30-36 (Canceled)

37. (Currently Amended) A method for determining the presence of a *Cryptosporidium parvum* organism in a test sample, said method comprising the steps of:

contacting ~~the~~ said test sample with said probe of claim 1 under stringent conditions; and

determining whether a probe:target hybrid has formed ~~under the stringent conditions~~ as an indication of the presence of a *Cryptosporidium parvum* organism in ~~the~~ said test sample.

38. (Currently Amended) The method of claim 37 further comprising providing to ~~the~~ said test sample a first amplification ~~primer~~ oligonucleotide under amplification conditions, said first ~~primer~~ amplification oligonucleotide comprising a target binding region from 18 to 40

bases in length that hybridizes to ~~an oligonucleotide having an at least 10 contiguous base region which is at least 80% complementary to an at least 10 contiguous base region present in~~ a target sequence selected from the group consisting of SEQ ID NO:48, SEQ ID NO:54, SEQ ID NO:60 and SEQ ID NO:66 under said amplification conditions, wherein said first amplification oligonucleotide does not comprise a base region in addition to said target binding region that is capable of stably binding to a target nucleic acid containing said target sequence under said amplification conditions, and wherein said ~~primer~~ first amplification oligonucleotide optionally includes a 5' sequence ~~which~~ that is recognized by an RNA polymerase or ~~which~~ that enhances initiation or elongation by an RNA polymerase.

39. (Currently Amended) The method of claim 38 further comprising providing to ~~the~~ said test sample a second amplification ~~primer~~ oligonucleotide under said amplification conditions, said second amplification oligonucleotide comprising a target binding region from 18 to 40 bases in length that hybridizes to ~~an oligonucleotide having an at least 10 contiguous base region which is at least 80% complementary to an at least 10 contiguous base region present in~~ a target sequence selected from the group consisting of SEQ ID NO:45, SEQ ID NO:51, SEQ ID NO:57 and SEQ ID NO:63 under said amplification conditions, wherein said second amplification oligonucleotide does not comprise a base region in addition to said target binding region that is capable of stably binding to a target nucleic acid containing said target sequence under said amplification conditions, and wherein said second amplification oligonucleotide optionally includes a 5' sequence that is recognized by an RNA polymerase or that enhances initiation or elongation by an RNA polymerase.

40. (Currently Amended) The method of claim 38 further comprising providing to ~~the~~ said test sample a second amplification ~~primer~~ oligonucleotide under amplification conditions, said second amplification oligonucleotide comprising a target binding region from 18 to 40 bases

in length that hybridizes to ~~an oligonucleotide having an at least 10 contiguous base region which is at least 80% complementary to an at least 10 contiguous base region present in~~ a target sequence selected from the group consisting of SEQ ID NO:46, SEQ ID NO:52, SEQ ID NO:58 and SEQ ID NO:64 under said amplification conditions, wherein said second amplification oligonucleotide does not comprise a base region in addition to said target binding region that is capable of stably binding to a target nucleic acid containing said target sequence under said amplification conditions, and wherein said second amplification oligonucleotide optionally includes a 5' sequence that is recognized by an RNA polymerase or that enhances initiation or elongation by an RNA polymerase.

Claims 41-49 (Canceled)

50. (Currently Amended) A method for determining the presence of a *Cryptosporidium parvum* organism in a test sample, said method comprising the steps of:

contacting ~~the~~ said test sample with said probe of claim 20 under stringent conditions; and

determining whether a probe:target hybrid has formed ~~under the stringent conditions~~ as an indication of the presence of a *Cryptosporidium parvum* organism in ~~the~~ said test sample.

51. (Currently Amended) A method for determining the presence of a *Cryptosporidium parvum* organism in a test sample, said method comprising the steps of:

contacting ~~the~~ said test sample with said probe of claim 21 under stringent conditions; and

determining whether a probe:target hybrid has formed ~~under the stringent conditions~~ as an indication of the presence of a *Cryptosporidium parvum* organism in ~~the~~ said test sample.

52. (Currently Amended) A method for determining the presence of a *Cryptosporidium parvum* organism in a test sample, said method comprising the steps of:

contacting ~~the~~ said test sample with said probe of claim 22 under stringent conditions; and

determining whether a probe:target hybrid has formed ~~under the stringent conditions~~ as an indication of the presence of a *Cryptosporidium parvum* organism in ~~the~~ said test sample.

53. (Currently Amended) A kit comprising, in packaged combination, first and second oligonucleotides for use in determining the presence of a *Cryptosporidium parvum* organism in a test sample, each of said oligonucleotides ~~having an at least 10 contiguous base region which is at least 80% complementary to an at least 10 contiguous base region present in~~ comprising a target binding region that hybridizes to a target sequence ~~contained~~ present in target nucleic acid derived from a *Cryptosporidium parvum* organism under hybridization conditions, said target binding region of said first oligonucleotide being from 18 to 35 bases in length and said target binding region of said second oligonucleotide being from 18 to 40 bases in length,

wherein: said the target sequence of said first oligonucleotide is selected from the group consisting of SEQ ID NO:6, SEQ ID NO:10, SEQ ID NO:14 and SEQ ID NO:18;

wherein said ~~the~~ target sequence of said second oligonucleotide is selected from the group consisting of SEQ ID NO:48, SEQ ID NO:54, SEQ ID NO:60 and SEQ ID NO:66;

wherein neither of said first and second oligonucleotides comprises a base region in addition to said target binding region that is capable of stably binding to said target nucleic acid under said conditions, and

wherein said second oligonucleotide optionally includes a 5' sequence ~~which~~ that is recognized by an RNA polymerase or ~~which~~ that enhances initiation or elongation by an RNA polymerase.

Claims 54-58 (Canceled)

59. (Currently Amended) The kit of claim 53 further comprising a third oligonucleotide, ~~wherein said third oligonucleotide has an at least 10 contiguous base region which is at least 80% complementary to an at least 10 contiguous base region present in~~ said third oligonucleotide comprising a target binding region from 18 to 40 bases in length that hybridizes to a target sequence ~~contained~~ present in target nucleic acid derived from a *Cryptosporidium parvum* organism under hybridization conditions, ~~and wherein the~~ said target sequence ~~of said third oligonucleotide is~~ being selected from the group consisting of SEQ ID NO:45, SEQ ID NO:51, SEQ ID NO:57 and SEQ ID NO:63, wherein said third oligonucleotide does not comprise a base region in addition to said target binding region that is capable of stably binding to said target nucleic acid under said conditions, and wherein said third oligonucleotide optionally includes a 5' sequence that is recognized by an RNA polymerase or that enhances initiation or elongation by an RNA polymerase.

60. (Currently Amended) The kit of claim 53 further comprising a third oligonucleotide, ~~wherein said third oligonucleotide has an at least 10 contiguous base region which is at least 80% complementary to an at least 10 contiguous base region present in~~ said third oligonucleotide comprising a target binding region from 18 to 40 bases in length that hybridizes to a target sequence ~~contained~~ present in target nucleic acid derived from a *Cryptosporidium parvum* organism under hybridization conditions, ~~and wherein the~~ said target sequence ~~of said third oligonucleotide is~~ being selected from the group consisting of SEQ ID NO:46, SEQ ID NO:52, SEQ ID NO:58 and SEQ ID NO:64, wherein said third oligonucleotide does not comprise a base region in addition to said target binding region that is capable of stably binding to said target nucleic acid under said conditions, and wherein said third oligonucleotide optionally includes a 5' sequence that

is recognized by an RNA polymerase or that enhances initiation or elongation by an RNA polymerase.

Claims 61-83 (Canceled)

84. (Currently Amended) A kit comprising, in packaged combination, first and second oligonucleotides for use in determining the presence of a *Cryptosporidium parvum* organism in a test sample, each of said oligonucleotides ~~having an at least 10 contiguous base region which is at least 80% complementary to an at least 10 contiguous base region present in~~ comprising a target binding region from 18 to 35 bases in length that hybridizes to a target sequence ~~contained~~ present in target nucleic acid derived from a *Cryptosporidium parvum* organism under stringent conditions,

wherein: said ~~the~~ target sequence of said first oligonucleotide is selected from the group consisting of SEQ ID NO:6, SEQ ID NO:10, SEQ ID NO:14 and SEQ ID NO:18,~~; and~~

wherein said ~~the~~ target sequence of said second oligonucleotide is selected from the group consisting of SEQ ID NO:29, SEQ ID NO:33, SEQ ID NO:37 and SEQ ID NO:41,

wherein neither of said first and second oligonucleotides comprises a base region in addition to said target binding region that is capable of stably binding to said target nucleic acid under said conditions, and

wherein said first oligonucleotide does not hybridize to nucleic acid derived from a *Cryptosporidium muris*, *Cryptosporidium baileyi* or *Cryptosporidium wrairi* organism to form a probe:non-target hybrid stable for detection under said conditions.

Claims 85-86 (Canceled)

87. (Withdrawn) The probe of claim 1, wherein the base sequence of said probe comprises the base sequence of SEQ ID NO:5, SEQ ID NO:9, SEQ ID NO:13 or SEQ ID NO:17.

88. (Withdrawn) The probe of claim 1, wherein the base sequence of said probe consists of or is contained within the base sequence of SEQ ID NO:5, SEQ ID NO:9, SEQ ID NO:13 or SEQ ID NO:17.

89. (Withdrawn) The probe of claim 1, wherein the base sequence of said probe consists of the base sequence of SEQ ID NO:5, SEQ ID NO:9, SEQ ID NO:13 or SEQ ID NO:17.

90. (Withdrawn) The probe of claim 1, wherein the base sequence of said probe comprises the base sequence of SEQ ID NO:7, SEQ ID NO:11, SEQ ID NO:15 or SEQ ID NO:19.

91. (Withdrawn) The probe of claim 1, wherein the base sequence of said probe consists of or is contained within the base sequence of SEQ ID NO:7, SEQ ID NO:11, SEQ ID NO:15 or SEQ ID NO:19.

92. (Withdrawn) The probe of claim 1, wherein the base sequence of said probe consists of the base sequence of SEQ ID NO:7, SEQ ID NO:11, SEQ ID NO:15 or SEQ ID NO:19.

93. (Currently Amended) The probe of claim 20, wherein ~~said oligonucleotide has~~ a the base sequence of said target binding region ~~which~~ is ~~100%~~ fully complementary to the base sequence of ~~the~~ said target sequence.

94. (Currently Amended) A probe mix comprising ~~the~~ said probe of claim 20 and a first helper oligonucleotide up to 35 bases in length and having a base sequence ~~which~~ that is at least 80% complementary to the base sequence of a target sequence selected from the group consisting of SEQ ID NO:29, SEQ ID NO:33, SEQ ID NO:37 and SEQ ID NO:41, wherein said first helper oligonucleotide hybridizes to said target sequence under stringent conditions.

95. (Currently Amended) The probe mix of claim 94 further comprising a second helper oligonucleotide up to 35 bases in length and having a base sequence ~~which~~ that is at least 80% complementary to the base sequence of a target sequence selected from the group consisting of SEQ ID NO:32, SEQ ID NO:36, SEQ ID NO:40 and SEQ ID NO:44, wherein said second helper oligonucleotide hybridizes to said target sequence under stringent conditions.

96. (Currently Amended) A probe mix comprising ~~the~~ said probe of claim 21 and a first helper oligonucleotide, wherein the base sequence of said first helper oligonucleotide is at least 80% complementary to the base sequence of a target sequence selected from the group consisting of SEQ ID NO:29, SEQ ID NO:33, SEQ ID NO:37 and SEQ ID NO:41, wherein said first helper oligonucleotide hybridizes to said target sequence under stringent conditions.

97. (Currently Amended) The probe mix of claim 96 further comprising a second helper oligonucleotide, wherein the base sequence of said second helper oligonucleotide is at least 80% complementary to the base sequence of a target sequence selected from the group consisting of SEQ ID NO:32, SEQ ID NO:36, SEQ ID NO:40 and SEQ ID NO:44, wherein said second helper oligonucleotide hybridizes to said target sequence under stringent conditions.

98. (Currently Amended) A probe mix comprising ~~the~~ said probe of claim 22 and a first helper oligonucleotide, wherein the base sequence of said first helper oligonucleotide is fully complementary to the base sequence of a target sequence selected from the group consisting of SEQ ID NO:29, SEQ ID NO:33, SEQ ID NO:37 and SEQ ID NO:41.

99. (Currently Amended) The probe mix of claim 98 further comprising a second helper oligonucleotide, wherein the base sequence of said second helper oligonucleotide is fully complementary to the base sequence of a target sequence selected from the group consisting of SEQ ID NO:32, SEQ ID NO:36, SEQ ID NO:40 and SEQ ID NO:44.

100. (Withdrawn) The probe mix of claim 23, wherein the base sequence of said probe comprises the base sequence of SEQ ID NO:5, SEQ ID NO:9, SEQ ID NO:13 or SEQ ID NO:17.

101. (Withdrawn) The probe mix of claim 23, wherein the base sequence of said probe consists of or is contained within the base sequence of SEQ ID NO:5, SEQ ID NO:9, SEQ ID NO:13 or SEQ ID NO:17.

102. (Withdrawn) The probe mix of claim 23, wherein the base sequence of said probe consists of the base sequence of SEQ ID NO:5, SEQ ID NO:9, SEQ ID NO:13 or SEQ ID NO:17.

103. (Withdrawn) The probe mix of claim 23, wherein the base sequence of said probe comprises the base sequence of SEQ ID NO:7, SEQ ID NO:11, SEQ ID NO:15 or SEQ ID NO:19.

104. (Withdrawn) The probe mix of claim 23, wherein the base sequence of said probe consists of or is contained within the base sequence of SEQ ID NO:7, SEQ ID NO:11, SEQ ID NO:15 or SEQ ID NO:19.

105. (Withdrawn) The probe mix of claim 23, wherein the base sequence of said probe consists of the base sequence of SEQ ID NO:7, SEQ ID NO:11, SEQ ID NO:15 or SEQ ID NO:19.

106. (Currently Amended) A probe mix comprising the probe of claim 93 and a first helper oligonucleotide up to 35 bases in length and having a base sequence ~~which~~ that is ~~100%~~ fully complementary to the base sequence of a target sequence selected from the group consisting of SEQ ID NO:29, SEQ ID NO:33, SEQ ID NO:37 and SEQ ID NO:41, wherein said first helper oligonucleotide hybridizes to said target sequence under stringent conditions.

107. (Currently Amended) The probe mix of claim 106 further comprising a second helper oligonucleotide up to 35 bases in length and having a base sequence ~~which~~ that is ~~100%~~ fully complementary to the base sequence of a target sequence selected from the group consisting of SEQ ID NO:32, SEQ ID NO:36, SEQ ID NO:40 and SEQ ID NO:44, wherein said second helper oligonucleotide hybridizes to said target sequence under stringent conditions.

108. (Withdrawn) The method of claim 37, wherein the base sequence of said probe comprises the base sequence of SEQ ID NO:5, SEQ ID NO:9, SEQ ID NO:13 or SEQ ID NO:17.

109. (Withdrawn) The method of claim 37, wherein the base sequence of said probe consists of or is contained within the base sequence of SEQ ID NO:5, SEQ ID NO:9, SEQ ID NO:13 or SEQ ID NO:17.

110. (Withdrawn) The method of claim 37, wherein the base sequence of said probe consists of the base sequence of SEQ ID NO:5, SEQ ID NO:9, SEQ ID NO:13 or SEQ ID NO:17.

111. (Withdrawn) The method of claim 37, wherein the base sequence of said probe comprises the base sequence of SEQ ID NO:7, SEQ ID NO:11, SEQ ID NO:15 or SEQ ID NO:19.

112. (Withdrawn) The method of claim 37, wherein the base sequence of said probe consists of or is contained within the base sequence of SEQ ID NO:7, SEQ ID NO:11, SEQ ID NO:15 or SEQ ID NO:19.

113. (Withdrawn) The method of claim 37, wherein the base sequence of said probe consists of the base sequence of SEQ ID NO:7, SEQ ID NO:11, SEQ ID NO:15 or SEQ ID NO:19.

114. (Currently Amended) The method of claim 50 further comprising providing to ~~the~~ said test sample a first amplification ~~primer~~ oligonucleotide under amplification conditions, said first ~~primer~~ amplification oligonucleotide comprising a target binding region from 18 to 40 bases in length that hybridizes to ~~an oligonucleotide having a base sequence~~ a target sequence ~~which is at least 80% complementary to a base sequence~~ selected from the group consisting of SEQ ID NO:48, SEQ ID NO:54, SEQ ID NO:60 and SEQ ID NO:66 under said amplification conditions, wherein said first amplification oligonucleotide does not comprise a base region in addition to said target binding region that is capable of stably binding to a target nucleic acid containing said target

sequence under said amplification conditions, and wherein said ~~primer~~ first amplification oligonucleotide optionally includes a 5' sequence ~~which~~ that is recognized by an RNA polymerase or ~~which~~ that enhances initiation or elongation by an RNA polymerase.

115. (Currently Amended) The method of claim 114 further comprising providing to ~~the~~ said test sample a second amplification primer oligonucleotide under said amplification conditions, said second amplification oligonucleotide comprising a target binding region from 18 to 40 bases in length that hybridizes to ~~an oligonucleotide having a base sequence~~ a target sequence ~~which is at least 80% complementary to a base sequence~~ selected from the group consisting of SEQ ID NO:45, SEQ ID NO:51, SEQ ID NO:57 and SEQ ID NO:63 under said amplification conditions, wherein said second amplification oligonucleotide does not comprise a base region in addition to said target binding region that is capable of stably binding to a target nucleic acid containing said target sequence under said amplification conditions, and wherein said second amplification oligonucleotide optionally includes a 5' sequence that is recognized by an RNA polymerase or that enhances initiation or elongation by an RNA polymerase.

116. (Currently Amended) The method of claim 114 further comprising providing to ~~the~~ said test sample a second amplification ~~primer~~ oligonucleotide under said amplification conditions, said second amplification oligonucleotide comprising a target binding region from 18 to 40 bases in length that hybridizes to ~~an oligonucleotide having a base sequence~~ a target sequence ~~which is at least 80% complementary to a base sequence~~ selected from the group consisting of SEQ ID NO:46, SEQ ID NO:52, SEQ ID NO:58 and SEQ ID NO:64 under said amplification conditions, wherein said second amplification oligonucleotide does not comprise a base region in addition to said target binding region that is capable of stably binding to a target nucleic acid containing said

target sequence under said amplification conditions, and wherein said second amplification oligonucleotide optionally includes a 5' sequence that is recognized by an RNA polymerase or that enhances initiation or elongation by an RNA polymerase.

117. (Currently Amended) The method of claim 50, wherein ~~said oligonucleotide has a~~ the base sequence ~~which~~ of said target binding region is ~~100%~~ fully complementary to the base sequence of ~~the~~ said target sequence.

118. (Currently Amended) The method of claim 117 further comprising providing to ~~the~~ said test sample a first amplification ~~primer~~ oligonucleotide comprising a target binding region under amplification conditions, wherein the base sequence of said ~~said first primer comprising~~ target binding region ~~an oligonucleotide having a base sequence which~~ is ~~100%~~ fully complementary to ~~a~~ the base sequence of a target sequence selected from the group consisting of SEQ ID NO:48, SEQ ID NO:54, SEQ ID NO:60 and SEQ ID NO:66,

wherein said target binding region hybridizes to said target sequence under said amplification conditions,

wherein said first amplification oligonucleotide does not comprise a base region in addition to said target binding region that is capable of stably binding to a target nucleic acid containing said target sequence under said amplification conditions, and

wherein said ~~primer~~ first amplification oligonucleotide optionally includes a 5' sequence ~~which~~ that is recognized by an RNA polymerase or ~~which~~ that enhances initiation or elongation by an RNA polymerase.

119. (Currently Amended) The method of claim 118 further comprising providing to ~~the~~ said test sample a second amplification ~~primer comprising~~ oligonucleotide comprising a target binding region under said amplification conditions, wherein the base sequence of said target binding

region ~~an oligonucleotide having a base sequence which~~ is ~~100%~~ fully complementary to ~~a~~ the base sequence of a target sequence selected from the group consisting of SEQ ID NO:45, SEQ ID NO:51, SEQ ID NO:57 and SEQ ID NO:63,

wherein said target binding region hybridizes to said target sequence under said amplification conditions,

wherein said second amplification oligonucleotide does not comprise a base region in addition to said target binding region that is capable of stably binding to a target nucleic acid containing said target sequence under said amplification conditions, and

wherein said second amplification oligonucleotide optionally includes a 5' sequence that is recognized by an RNA polymerase or that enhances initiation or elongation by an RNA polymerase.

120. (Currently Amended) The method of claim 118 further comprising providing to ~~the~~ said test sample a second amplification ~~primer comprising~~ oligonucleotide comprising a target binding region under said amplification conditions, wherein the base sequence of said target binding region ~~an oligonucleotide having a base sequence which~~ is ~~100%~~ fully complementary to ~~a~~ the base sequence of a target sequence selected from the group consisting of SEQ ID NO:46, SEQ ID NO:52, SEQ ID NO:58 and SEQ ID NO:64,

wherein said target binding region hybridizes to said target sequence under said amplification conditions,

wherein said second amplification oligonucleotide does not comprise a base region in addition to said target binding region that is capable of stably binding to a target nucleic acid containing said target sequence under said amplification conditions, and

wherein said second amplification oligonucleotide optionally includes a 5' sequence that is recognized by an RNA polymerase or that enhances initiation or elongation by an RNA polymerase.

121. (Currently Amended) The method of claim 51 further comprising providing to ~~the~~ said test sample a first amplification ~~primer~~ oligonucleotide comprising a target binding region under amplification conditions, wherein the base sequence of said ~~first primer~~ target binding region is at least 80% complementary to ~~a~~ the base sequence of a target sequence selected from the group consisting of SEQ ID NO:48, SEQ ID NO:54, SEQ ID NO:60 and SEQ ID NO:66,

wherein said target binding region hybridizes to said target sequence under said amplification conditions,

wherein said first amplification oligonucleotide does not comprise a base region in addition to said target binding region that is capable of stably binding to a target nucleic acid containing said target sequence under said amplification conditions, and

wherein said ~~primer~~ first amplification oligonucleotide optionally includes a 5' sequence ~~which~~ that is recognized by an RNA polymerase or ~~which~~ that enhances initiation or elongation by an RNA polymerase.

122. (Currently Amended) The method of claim 121 further comprising providing to ~~the~~ said test sample a second amplification ~~primer~~ oligonucleotide comprising a target binding region under amplification conditions, wherein the base sequence of said ~~second primer~~ target binding regon is at least 80% complementary to ~~a~~ the base sequence of a target sequence selected from the group consisting of SEQ ID NO:45, SEQ ID NO:51, SEQ ID NO:57 and SEQ ID NO:63,

wherein said target binding region hybridizes to said target sequence under said amplification conditions,

wherein said second amplification oligonucleotide does not comprise a base region in addition to said target binding region that is capable of stably binding to a target nucleic acid containing said target sequence under said amplification conditions, and

wherein said second amplification oligonucleotide optionally includes a 5' sequence that is recognized by an RNA polymerase or that enhances initiation or elongation by an RNA polymerase.

123. (Currently Amended) The method of claim 121 further comprising providing to ~~the~~ said test sample a second amplification ~~primer~~ oligonucleotide comprising a target binding region under amplification conditioins, wherein the base sequence of said ~~second primer~~ target binding region is at least 80% complementary to ~~a~~ the base sequence of a target sequence selected from the group consisting of SEQ ID NO:46, SEQ ID NO:52, SEQ ID NO:58 and SEQ ID NO:64,

wherein said target binding region hybridizes to said target sequence under said amplification conditions,

wherein said second amplification oligonucleotide does not comprise a base region in addition to said target binding region that is capable of stably binding to a target nucleic acid containing said target sequence under said amplification conditions, and

wherein said second amplification oligonucleotide optionally includes a 5' sequence that is recognized by an RNA polymerase or that enhances initiation or elongation by an RNA polymerase.

124. (Currently Amended) The method of claim 52 further comprising providing to ~~the~~ said test sample a first amplification ~~primer~~ oligonucleotide comprising a target binding region under amplification conditions, wherein the base sequence of said ~~first primer~~ target binding region is fully complementary to ~~a~~ the base sequence of a target sequence selected from the group consisting of SEQ ID NO:48, SEQ ID NO:54, SEQ ID NO:60 and SEQ ID NO:66,

wherein said target binding region hybridizes to said target sequence under said amplification conditions,

wherein said first amplification oligonucleotide does not comprise a base region in addition to said target binding region that is capable of stably binding to a target nucleic acid containing said target sequence under said amplification conditions, and

wherein said ~~primer~~ first amplification oligonucleotide optionally includes a 5' sequence ~~which~~ that is recognized by an RNA polymerase or ~~which~~ that enhances initiation or elongation by an RNA polymerase.

125. (Currently Amended) The method of claim 124 further comprising providing to ~~the~~ said test sample a second amplification ~~primer~~ oligonucleotide comprising a target binding region under amplification conditions, wherein the base sequence of said target binding region ~~second primer~~ is fully complementary to a the base sequence of a target sequence selected from the group consisting of SEQ ID NO:45, SEQ ID NO:51, SEQ ID NO:57 and SEQ ID NO:63,

wherein said target binding region hybridizes to said target sequence under said amplification conditions,

wherein said second amplification oligonucleotide does not comprise a base region in addition to said target binding region that is capable of stably binding to a target nucleic acid containing said target sequence under said amplification conditions, and

wherein said second amplification oligonucleotide optionally includes a 5' sequence that is recognized by an RNA polymerase or that enhances initiation or elongation by an RNA polymerase.

126. (Currently Amended) The method of claim 124 further comprising providing to ~~the~~ said test sample a second amplification ~~primer~~ oligonucleotide comprising a target binding region under amplification conditions, wherein the base sequence of said target binding region ~~second primer~~ is fully complementary to a the base sequence of a target sequence selected from the group consisting of SEQ ID NO:46, SEQ ID NO:52, SEQ ID NO:58 and SEQ ID NO:64,

wherein said target binding region hybridizes to said target sequence under said amplification conditions,

wherein said second amplification oligonucleotide does not comprise a base region in addition to said target binding region that is capable of stably binding to a target nucleic acid containing said target sequence under said amplification conditions, and

wherein said second amplification oligonucleotide optionally includes a 5' sequence that is recognized by an RNA polymerase or that enhances initiation or elongation by an RNA polymerase.

127. (Withdrawn) The kit of claim 53, wherein the base sequence of said first oligonucleotide comprises the base sequence of SEQ ID NO:5, SEQ ID NO:9, SEQ ID NO:13 or SEQ ID NO:17.

128. (Withdrawn) The kit of claim 53, wherein the base sequence of said first oligonucleotide consists of or is contained within the base sequence of SEQ ID NO:5, SEQ ID NO:9, SEQ ID NO:13 or SEQ ID NO:17.

129. (Withdrawn) The kit of claim 53, wherein the base sequence of said first oligonucleotide consists of the base sequence of SEQ ID NO:5, SEQ ID NO:9, SEQ ID NO:13 or SEQ ID NO:17.

130. (Withdrawn) The kit of claim 53, wherein the base sequence of said first oligonucleotide comprises the base sequence of SEQ ID NO:7, SEQ ID NO:11, SEQ ID NO:15 or SEQ ID NO:19.

131. (Withdrawn) The kit of claim 53, wherein the base sequence of said first oligonucleotide consists of or is contained within the base sequence of SEQ ID NO:7, SEQ ID NO:11, SEQ ID NO:15 or SEQ ID NO:19.

132. (Withdrawn) The kit of claim 53, wherein the base sequence of said first oligonucleotide consists of the base sequence of SEQ ID NO:7, SEQ ID NO:11, SEQ ID NO:15 or SEQ ID NO:19.

133. (Currently Amended) The kit of claim 53, wherein the base sequence of said target binding region of each ~~of~~ said ~~oligonucleotides has a base region which~~ oligonucleotide is at least 80% complementary to the base sequence of ~~the~~ said target sequence of said oligonucleotide.

134. (Currently Amended) The kit of claim 53, wherein the base sequence of each said target binding region of each ~~of~~ said ~~oligonucleotides has a base region which~~ oligonucleotide is ~~100%~~ fully complementary to the base sequence of ~~the~~ said target sequence of said oligonucleotide.

135. (Currently Amended) The kit of claim 53, wherein the base sequence of each ~~of~~ said oligonucleotide ~~oligonucleotides~~ is at least 80% complementary to the base sequence of the said target sequence of said oligonucleotide.

136. (Currently Amended) The kit of claim 53, wherein the base sequence of each ~~of~~ said oligonucleotide ~~oligonucleotides~~ is fully complementary to the base sequence of ~~the~~ said target sequence of said oligonucleotide.

137. (Currently Amended) The kit of claim 59, wherein the base sequence of said target binding region of each ~~of~~ said ~~oligonucleotides has a base region which~~ oligonucleotide is at least 80% complementary to the base sequence of ~~the~~ said target sequence of said oligonucleotide.

138. (Currently Amended) The kit of claim 59, wherein the base sequence of said target binding region of each ~~of~~ said ~~oligonucleotides has a base region which~~ oligonucleotide is ~~100%~~ fully complementary to the base sequence of ~~the~~ said target sequence of said oligonucleotide.

139. (Currently Amended) The kit of claim 59, wherein the base sequence of each ~~of~~ said oligonucleotide ~~oligonucleotides~~ is at least 80% complementary to the base sequence of ~~the~~ said target sequence of said oligonucleotide.

140. (Currently Amended) The kit of claim 59, wherein the base sequence of each ~~of~~ said oligonucleotide ~~oligonucleotides~~ is fully complementary to the base sequence of ~~the~~ said target sequence of said oligonucleotide.

141. (Currently Amended) The kit of claim 60, wherein the base sequence of said target binding region of each ~~of~~ said ~~oligonucleotides has a base region which~~ oligonucleotide is at least 80% complementary to the base sequence of ~~the~~ said target sequence of said oligonucleotide.

142. (Currently Amended) The kit of claim 60, wherein the base sequence of said target binding region of each ~~of~~ said ~~oligonucleotides has a base region which~~ oligonucleotide is ~~100%~~ fully complementary to the base sequence of ~~the~~ said target sequence of said oligonucleotide.

143. (Currently Amended) The kit of claim 60, wherein the base sequence of each ~~of~~ said ~~oligonucleotides~~ oligonucleotide is at least 80% complementary to the base sequence of ~~the~~ said target sequence of said oligonucleotide.

144. (Currently Amended) The kit of claim 60, wherein the base sequence of each ~~of~~ said ~~oligonucleotides~~ oligonucleotide is fully complementary to the base sequence of ~~the~~ said target sequence of said oligonucleotide.

145. (Withdrawn) The kit of claim 84, wherein the base sequence of said first oligonucleotide comprises the base sequence of SEQ ID NO:5, SEQ ID NO:9, SEQ ID NO:13 or SEQ ID NO:17.

146. (Withdrawn) The kit of claim 84, wherein the base sequence of said first oligonucleotide consists of or is contained within the base sequence of SEQ ID NO:5, SEQ ID NO:9, SEQ ID NO:13 or SEQ ID NO:17.

147. (Withdrawn) The kit of claim 84, wherein the base sequence of said first oligonucleotide consists of the base sequence of SEQ ID NO:5, SEQ ID NO:9, SEQ ID NO:13 or SEQ ID NO:17.

148. (Withdrawn) The kit of claim 84, wherein the base sequence of said first oligonucleotide comprises the base sequence of SEQ ID NO:7, SEQ ID NO:11, SEQ ID NO:15 or SEQ ID NO:19.

149. (Withdrawn) The kit of claim 84, wherein the base sequence of said first oligonucleotide consists of or is contained within the base sequence of SEQ ID NO:7, SEQ ID NO:11, SEQ ID NO:15 or SEQ ID NO:19.

150. (Withdrawn) The kit of claim 84, wherein the base sequence of said first oligonucleotide consists of the base sequence of SEQ ID NO:7, SEQ ID NO:11, SEQ ID NO:15 or SEQ ID NO:19.

151. (Currently Amended) The kit of claim 84, wherein the base sequence of said target binding region of each ~~of said oligonucleotides has a base region which~~ oligonucleotide is at least 80% complementary to the base sequence of ~~the~~ said target sequence of said oligonucleotide.

152. (Currently Amended) The kit of claim 84, wherein the base sequence of said target binding region of each ~~of said oligonucleotides has a base region which~~ oligonucleotide is ~~100%~~ fully complementary to the base sequence of ~~the~~ said target sequence of said oligonucleotide.

153. (Currently Amended) The kit of claim 84, wherein the base sequence of each of said oligonucleotide ~~oligonucleotides~~ is at least 80% complementary to the base sequence of ~~the~~ said target sequence of said oligonucleotide.

154. (Currently Amended) The kit of claim 84, wherein the base sequence of each ~~of~~ said oligonucleotide ~~oligonucleotides~~ is fully complementary to the base sequence of ~~the~~ said target sequence of said oligonucleotide.

155. (Currently Amended) The kit of claim 84 further comprising a third oligonucleotide comprising a target binding region from 18 to 35 bases in length that hybridizes to;

~~wherein said third oligonucleotide has an at least 10 contiguous base region which is at least 80% complementary to an at least 10 contiguous base region present in~~ a target sequence ~~contained~~ present in target nucleic acid derived from a *Cryptosporidium parvum* organism under stringent conditions, ~~and wherein the~~ said target sequence ~~of said third oligonucleotide is~~ being selected from the group consisting of SEQ ID NO:32, SEQ ID NO:36, SEQ ID NO:40 and SEQ ID NO:44.

156. (Currently Amended) The kit of claim 155, wherein each ~~of~~ said oligonucleotide ~~oligonucleotides~~ has a base region ~~which~~ that is at least 80% complementary to the base sequence of ~~the~~ said target sequence of said oligonucleotide.

157. (Currently Amended) The kit of claim 155, wherein each ~~of~~ said oligonucleotide ~~oligonucleotides~~ has a base region ~~which~~ that is ~~100%~~ fully complementary to the base sequence of ~~the~~ said target sequence of said oligonucleotide.

158. (Currently Amended) The kit of claim 155, wherein the base sequence of each ~~of~~ said oligonucleotide ~~oligonucleotides~~ is at least 80% complementary to the base sequence of ~~the~~ said target sequence of said oligonucleotide.

159. (Currently Amended) The kit of claim 155, wherein the base sequence of each of said oligonucleotide ~~oligonucleotides~~ is fully complementary to the base sequence of ~~the~~ said target sequence of said oligonucleotide.